

WO 2005/001480

PCT/AU2004/000856

1

SEQUENCE LISTING

<110> Proteome Systems Intellectual Propoerty Pty Ltd

5 <120> Method of isolating a protein

<130> 502469/PXM

<160> 26

10 <170> PatentIn version 3.1

<210> 1

<211> 593

15 <212> PRT

<213> protein G

<400> 1

20 Met Glu Lys Glu Lys Lys Val Lys Tyr Phe Leu Arg Lys Ser Ala Phe  
1 5 10 15

25 Gly Leu Ala Ser Val Ser Ala Ala Phe Leu Val Gly Ser Thr Val Phe  
20 25 30

Ala Val Asp Ser Pro Ile Glu Asp Thr Pro Ile Ile Arg Asn Gly Gly  
35 40 45

30 Glu Leu Thr Asn Leu Leu Gly Asn Ser Glu Thr Thr Leu Ala Leu Arg  
50 55 60

35 Asn Glu Glu Ser Ala Thr Ala Asp Leu Thr Ala Ala Ala Val Ala Asp  
65 70 75 80

40 Thr Val Ala Ala Ala Ala Ala Glu Asn Ala Gly Ala Ala Ala Trp Glu  
85 90 95

45 Ala Ala Ala Ala Ala Asp Ala Leu Ala Lys Ala Lys Ala Asp Ala Leu  
100 105 110

Lys Glu Phe Asn Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile  
115 120 125

50 Asn Asn Ala Lys Thr Val Glu Gly Val Lys Asp Leu Gln Ala Gln Val  
130 135 140

55 Val Glu Ser Ala Lys Lys Ala Arg Ile Ser Glu Ala Thr Asp Gly Leu  
145 150 155 160

60 Ser Asp Phe Leu Lys Ser Gln Thr Pro Ala Glu Asp Thr Val Lys Ser  
165 170 175

Ile Glu Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys

	180	185	190
5	Tyr Gly Val Ser Asp Tyr His Lys Asn Leu Ile Asn Asn Ala Lys Thr 195 200 205		
10	Val Glu Gly Val Lys Asp Leu Gln Ala Gln Val Val Glu Ser Ala Lys 210 215 220		
15	Lys Ala Arg Ile Ser Glu Ala Thr Asp Gly Leu Ser Asp Phe Leu Lys 225 230 235 240		
20	Ser Gln Thr Pro Ala Glu Asp Thr Val Lys Ser Ile Glu Leu Ala Glu 245 250 255		
25	Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp 260 265 270		
30	Tyr Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys 275 280 285		
35	Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro Lys Thr Asp Thr Tyr 290 295 300		
40	Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Glu 305 310 315 320		
45	Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn 325 330 335		
50	Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr 340 345 350		
55	Phe Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala Ser Glu Leu Thr 355 360 365		
60	Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu Lys 370 375 380		
	Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val 385 390 395 400		
	Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr 405 410 415		
	Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile 420 425 430		
	Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile		

435                      440                      445  
 5    Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala  
      450                      455                      460  
 10    Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val  
      465                      470                      475                      480  
      Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr  
                                  485                      490                      495  
 15    Glu Met Val Thr Glu Val Pro Gly Asp Ala Pro Thr Glu Pro Glu Lys  
                                  500                      505                      510  
 20    Pro Glu Ala Ser Ile Pro Leu Val Pro Leu Thr Pro Ala Thr Pro Ile  
                                  515                      520                      525  
 25    Ala Lys Asp Asp Ala Lys Lys Asp Asp Thr Lys Lys Glu Asp Ala Lys  
      530                      535                      540  
 30    Lys Pro Glu Ala Lys Lys Glu Asp Ala Lys Lys Ala Glu Thr Leu Pro  
      545                      550                      555                      560  
      Thr Thr Gly Glu Gly Ser Asn Pro Phe Phe Thr Ala Ala Ala Leu Ala  
                                  565                      570                      575  
 35    Val Met Ala Gly Ala Gly Ala Leu Ala Val Ala Ser Lys Arg Lys Glu  
                                  580                      585                      590  
 40    Asp  
 45    <210> 2  
      <211> 454  
      <212> PRT  
      <213> protein A  
 50    <400> 2  
      Met Met Thr Leu Gln Ile His Thr Gly Gly Ile Asn Leu Lys Lys Lys  
      1                      5                      10                      15  
 55    Asn Ile Tyr Ser Ile Arg Lys Leu Gly Val Gly Ile Ala Ser Val Thr  
                                  20                      25                      30  
 60    Leu Gly Thr Leu Leu Ile Ser Gly Gly Val Thr Pro Ala Ala Asn Ala  
      35                      40                      45  
      Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu Asn  
      50                      55                      60

5 Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu  
 65 70 75 80  
 Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys  
 85 90 95  
 10 Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln Gln Asn Lys Phe  
 100 105 110  
 15 Asn Lys Asp Gln Gln Ser Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn  
 115 120 125  
 20 Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp  
 130 135 140  
 Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala Lys Lys Leu Asn Glu  
 145 150 155 160  
 25 Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys Glu Gln Gln Asn  
 165 170 175  
 30 Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg  
 180 185 190  
 35 Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn  
 195 200 205  
 40 Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala  
 210 215 220  
 Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu  
 225 230 235 240  
 45 His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser  
 245 250 255  
 50 Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys  
 260 265 270  
 55 Lys Leu Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro  
 275 280 285  
 60 Gly Lys Glu Asp Asn Asn Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro  
 290 295 300  
 Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro  
 305 310 315 320

Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro  
 325 330 335  
 5  
 Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro  
 340 345 350  
 10  
 Gly Lys Glu Asp Gly Asn Gly Val His Val Val Lys Pro Gly Asp Thr  
 355 360 365  
 15 Val Asn Asp Ile Ala Lys Ala Asn Gly Thr Thr Ala Asp Lys Ile Ala  
 370 375 380  
 20 Val Asp Asn Lys Leu Ala Asp Lys Asn Met Ile Lys Pro Gly Gln Glu  
 385 390 395 400  
 Leu Val Val Asp Lys Lys Gln Pro Ala Asn His Ala Asp Ala Asn Lys  
 405 410 415  
 25  
 Ala Gln Ala Leu Pro Glu Thr Gly Glu Glu Asn Pro Phe Ile Gly Thr  
 420 425 430  
 30  
 Thr Val Phe Gly Gly Leu Ser Leu Ala Leu Gly Ala Ala Leu Leu Ala  
 435 440 445  
 35 Gly Arg Arg Arg Glu Leu  
 450  
 40 <210> 3  
 <211> 719  
 <212> PRT  
 <213> protein L  
 <400> 3  
 45 Met Ala Ala Leu Ala Gly Ala Ile Val Val Thr Gly Gly Val Gly Ser  
 1 5 10 15  
 50 Tyr Ala Ala Asp Glu Pro Ile Asp Leu Glu Lys Leu Glu Glu Lys Arg  
 20 25 30  
 55 Asp Lys Glu Asn Val Gly Asn Leu Pro Lys Phe Asp Asn Glu Val Lys  
 35 40 45  
 Asp Gly Ser Glu Asn Pro Met Ala Lys Tyr Pro Asp Phe Asp Asp Glu  
 50 55 60  
 60 Ala Ser Thr Arg Phe Glu Thr Glu Asn Asn Glu Phe Glu Glu Lys Lys  
 65 70 75 80

Val Val Ser Asp Asn Phe Phe Asp Gln Ser Glu His Pro Phe Val Glu  
 85 90 95  
 5 Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu  
 100 105 110  
 10 Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr  
 115 120 125  
 15 Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala  
 130 135 140  
 20 Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val  
 145 150 155 160  
 Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys  
 165 170 175  
 25 Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile  
 180 185 190  
 30 Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu  
 195 200 205  
 35 Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp  
 210 215 220  
 40 Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn  
 225 230 235 240  
 Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu  
 245 250 255  
 45 Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr  
 260 265 270  
 50 Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg  
 275 280 285  
 55 Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val  
 290 295 300  
 60 Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys  
 305 310 315 320  
 Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile  
 325 330 335

Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Ala  
 340 345 350  
 5  
 Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu  
 355 360 365  
 10 Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr Thr Ile Asn  
 370 375 380  
 15 Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu Glu Lys Glu  
 385 390 395 400  
 20 Gln Val Thr Ile Lys Glu Asn Ile Tyr Phe Glu Asp Gly Thr Val Gln  
 405 410 415  
 25 Thr Ala Thr Phe Lys Gly Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr  
 420 425 430  
 Arg Tyr Ala Asp Leu Leu Ser Lys Glu His Gly Lys Tyr Thr Ala Asp  
 435 440 445  
 30 Leu Glu Asp Gly Gly Tyr Thr Ile Asn Ile Arg Phe Ala Gly Lys Glu  
 450 455 460  
 35 Glu Pro Glu Glu Thr Pro Glu Lys Pro Glu Val Gln Asp Gly Tyr Ala  
 465 470 475 480  
 40 Ser Tyr Glu Glu Ala Glu Ala Ala Ala Lys Glu Ala Leu Lys Asn Asp  
 485 490 495  
 Asp Val Asn Lys Ser Tyr Thr Ile Arg Gln Gly Ala Asp Gly Arg Tyr  
 500 505 510  
 45 Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Glu Glu Lys Pro Glu Ala  
 515 520 525  
 50 Gln Asn Gly Tyr Ala Thr Tyr Glu Glu Ala Glu Ala Ala Ala Lys Lys  
 530 535 540  
 55 Ala Leu Glu Asn Asp Pro Ile Asn Lys Ser Tyr Ser Ile Arg Gln Gly  
 545 550 555 560  
 60 Ala Asp Gly Arg Tyr Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Thr  
 565 570 575  
 Pro Glu Lys Pro Val Glu Pro Ser Glu Pro Ser Thr Pro Asp Val Pro  
 580 585 590

Ser Asn Pro Ser Asn Pro Ser Thr Pro Asp Val Pro Ser Thr Pro Asp  
 595 600 605  
 5 Val Pro Ser Asn Pro Ser Thr Pro Glu Val Pro Ser Asn Pro Ser Thr  
 610 615 620  
 10 Pro Gly Asn Glu Glu Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu  
 625 630 635 640  
 15 Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly  
 645 650 655  
 Asn Glu Gln Lys Pro Asp Gln Pro Ser Lys Pro Glu Lys Glu Glu Asn  
 660 665 670  
 20 Gly Lys Gly Gly Val Asp Ser Pro Lys Lys Lys Glu Lys Ala Ala Leu  
 675 680 685  
 25 Pro Lys Ala Gly Ser Glu Ala Glu Ile Leu Thr Leu Ala Ala Ala Ser  
 690 695 700  
 30 Leu Ser Ser Val Ala Gly Ala Phe Ile Ser Leu Lys Lys Arg Lys  
 705 710 715  
 35 <210> 4  
 <211> 20  
 <212> PRT  
 <213> protein A mimetic  
 <400> 4  
 40 Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn  
 1 5 10 15  
 45 Glu Glu Gln Arg  
 20  
 50 <210> 5  
 <211> 16  
 <212> PRT  
 <213> protein A mimetic  
 <400> 5  
 55 Arg Thr Tyr Arg Thr Tyr Arg Thr Tyr Arg Thr Tyr Lys Lys Lys Gly  
 1 5 10 15  
 60 <210> 6  
 <211> 18  
 <212> PRT  
 <213> fragment of M. tuberculosis glutamine synthetase



<400> 6  
Phe Glu Ala Val Lys Gly Glu Cys Asn Met Gly Gln Gln Glu Ile Gly  
1 5 10 15  
5  
Phe Arg  
10  
<210> 7  
<211> 15  
<212> PRT  
<213> fragment of M. tuberculosis glutamine synthetase .  
15  
<400> 7  
Glu Ile Ala Asp Gln His Gly Lys Ser Leu Thr Phe Met Ala Lys  
1 5 10 15  
20  
<210> 8  
<211> 14  
<212> PRT  
25 <213> fragment of M. tuberculosis glutamine synthetase  
<400> 8  
Glu Phe Thr Leu Cys Tyr Ala Pro Thr Ile Asn Ser Tyr Lys  
1 5 10  
30  
<210> 9  
<211> 9  
35 <212> PRT  
<213> fragment of M. tuberculosis glutamine synthetase  
<400> 9  
40 Val Val Gly His Gly Gln Asn Ile Arg  
1 5  
45  
<210> 10  
<211> 19  
<212> PRT  
<213> fragment of M. tuberculosis glutamine synthetase  
<400> 10  
50  
Leu Pro Val Thr Leu Ala Asp Ala Ala Val Leu Phe Glu Asp Ser Ala  
1 5 10 15  
55 Leu Val Arg  
60  
<210> 11  
<211> 15  
<212> PRT  
<213> fragment of M. tuberculosis glutamine synthetase  
<400> 11

10

Val Glu Leu Ala Ala Phe Asn Ala Ala Val Thr Asp Trp Glu Arg  
 1 5 10 15  
 5  
 <210> 12  
 <211> 457  
 <212> PRT  
 <213> M. tuberculosis glutamine synthetase  
 10  
 <400> 12  
 Met Thr Gly Pro Gly Ser Pro Pro Leu Ala Trp Thr Glu Leu Glu Arg  
 1 5 10 15  
 15  
 Leu Val Ala Ala Gly Asp Val Asp Thr Val Ile Val Ala Phe Thr Asp  
 20 25 30  
 20  
 Met Gln Gly Arg Leu Ala Gly Lys Arg Ile Ser Gly Arg His Phe Val  
 35 40 45  
 25  
 Asp Asp Ile Ala Thr Arg Gly Val Glu Cys Cys Ser Tyr Leu Leu Ala  
 50 55 60  
 30  
 Val Asp Val Asp Leu Asn Thr Val Pro Gly Tyr Ala Met Ala Ser Trp  
 65 70 75 80  
 35  
 Asp Thr Gly Tyr Gly Asp Met Val Met Thr Pro Asp Leu Ser Thr Leu  
 85 90 95  
 40  
 Arg Leu Ile Pro Trp Leu Pro Gly Thr Ala Leu Val Ile Ala Asp Leu  
 100 105 110  
 40  
 Val Trp Ala Asp Gly Ser Glu Val Ala Val Ser Pro Arg Ser Ile Leu  
 115 120 125  
 45  
 Arg Arg Gln Leu Asp Arg Leu Lys Ala Arg Gly Leu Val Ala Asp Val  
 130 135 140  
 50  
 Ala Thr Glu Leu Glu Phe Ile Val Phe Asp Gln Pro Tyr Arg Gln Ala  
 145 150 155 160  
 55  
 Trp Ala Ser Gly Tyr Arg Gly Leu Thr Pro Ala Ser Asp Tyr Asn Ile  
 165 170 175  
 Asp Tyr Ala Ile Leu Ala Ser Ser Arg Met Glu Pro Leu Leu Arg Asp  
 180 185 190  
 60  
 Ile Arg Leu Gly Met Ala Gly Ala Gly Leu Arg Phe Glu Ala Val Lys  
 195 200 205

Gly Glu Cys Asn Met Gly Gln Gln Glu Ile Gly Phe Arg Tyr Asp Glu  
 210 215 220

5 Ala Leu Val Thr Cys Asp Asn His Ala Ile Tyr Lys Asn Gly Ala Lys  
 225 230 235 240

10 Glu Ile Ala Asp Gln His Gly Lys Ser Leu Thr Phe Met Ala Lys Tyr  
 245 250 255

15 Asp Glu Arg Glu Gly Asn Ser Cys His Ile His Val Ser Leu Arg Gly  
 260 265 270

Thr Asp Gly Ser Ala Val Phe Ala Asp Ser Asn Gly Pro His Gly Met  
 275 280 285

20 Ser Ser Met Phe Arg Ser Phe Val Ala Gly Gln Leu Ala Thr Leu Arg  
 290 295 300

25 Glu Phe Thr Leu Cys Tyr Ala Pro Thr Ile Asn Ser Tyr Lys Arg Phe  
 305 310 315 320

30 Ala Asp Ser Ser Phe Ala Pro Thr Ala Leu Ala Trp Gly Leu Asp Asn  
 325 330 335

35 Arg Thr Cys Ala Leu Arg Val Val Gly His Gly Gln Asn Ile Arg Val  
 340 345 350

Glu Cys Arg Val Pro Gly Gly Asp Val Asn Gln Tyr Leu Ala Val Ala  
 355 360 365

40 Ala Leu Ile Ala Gly Gly Leu Tyr Gly Ile Glu Arg Gly Leu Gln Leu  
 370 375 380

45 Pro Glu Pro Cys Val Gly Asn Ala Tyr Gln Gly Ala Asp Val Glu Arg  
 385 390 395 400

50 Leu Pro Val Thr Leu Ala Asp Ala Ala Val Leu Phe Glu Asp Ser Ala  
 405 410 415

Leu Val Arg Glu Ala Phe Gly Glu Asp Val Val Ala His Tyr Leu Asn  
 420 425 430

55 Asn Ala Arg Val Glu Leu Ala Ala Phe Asn Ala Ala Val Thr Asp Trp  
 435 440 445

60 Glu Arg Ile Arg Gly Phe Glu Arg Leu  
 450 455

<210> 13  
 <211> 1191  
 <212> DNA  
 <213> M. tuberculosis Elongation Factor TU

5

<220>  
 <221> CDS  
 <222> (1)..(1191)  
 <223>

10

<400> 13  
 gtg gcg aag gcg aag ttc cag cgg acc aag ccc cac gtc aac atc ggg 48  
 Val Ala Lys Ala Lys Phe Gln Arg Thr Lys Pro His Val Asn Ile Gly  
 1 5 10 15

15

acc atc ggt cac gtt gac cac ggc aag acc acc ctg acc gcg gct atc 96  
 Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile  
 20 25 30

20

acc aag gtc ctg cac gac aaa ttc ccc gat ctg aac gag acg aag gca 144  
 Thr Lys Val Leu His Asp Lys Phe Pro Asp Leu Asn Glu Thr Lys Ala  
 35 40 45

25

ttc gac cag atc gac aac gcc ccc gag gag cgt cag cgc ggt atc acc 192  
 Phe Asp Gln Ile Asp Asn Ala Pro Glu Glu Arg Gln Arg Gly Ile Thr  
 50 55 60

30

atc aac atc gcg cac gtg gag tac cag acc gac aag cgg cac tac gca 240  
 Ile Asn Ile Ala His Val Glu Tyr Gln Thr Asp Lys Arg His Tyr Ala  
 65 70 75 80

35

cac gtc gac gcc cct ggc cac gcc gac tac atc aag aac atg atc acc 288  
 His Val Asp Ala Pro Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr  
 85 90 95

40

ggc gcc gcg cag atg gac ggt gcg atc ctg gtg gtc gcc gcc acc gac 336  
 Gly Ala Ala Gln Met Asp Gly Ala Ile Leu Val Val Ala Thr Asp  
 100 105 110

45

ggc ccg atg ccc cag acc cgc gag cac gtt ctg ctg gcg cgt caa gtg 384  
 Gly Pro Met Pro Gln Thr Arg Glu His Val Leu Leu Ala Arg Gln Val  
 115 120 125

50

ggt gtg ccc tac atc ctg gta gcg ctg aac aag gcc gac gca gtg gac 432  
 Gly Val Pro Tyr Ile Leu Val Ala Leu Asn Lys Ala Asp Ala Val Asp  
 130 135 140

55

gac gag gag ctg ctc gaa ctc gtc gag atg gag gtc cgc gag ctg ctg 480  
 Asp Glu Glu Leu Leu Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu  
 145 150 155 160

60

gct gcc cag gaa ttc gac gag gac gcc ccg gtt gtg cgg gtc tcg gcg 528  
 Ala Ala Gln Glu Phe Asp Glu Asp Ala Pro Val Val Arg Val Ser Ala  
 165 170 175

65

ctc aag gcg ctc gag ggt gac gcg aag tgg gtt gcc tct gtc gag gaa 576  
 Leu Lys Ala Leu Glu Gly Asp Ala Lys Trp Val Ala Ser Val Glu Glu  
 180 185 190

70

ctg atg aac gcg gtc gac gag tcg att ccg gac ccg gtc cgc gag acc 624  
 Leu Met Asn Ala Val Asp Glu Ser Ile Pro Asp Pro Val Arg Glu Thr  
 195 200 205

75

gac aag ccg ttc ctg atg ccg gtc gag gac gtc ttc acc att acc ggc 672

	Asp	Lys	Pro	Phe	Leu	Met	Pro	Val	Glu	Asp	Val	Phe	Thr	Ile	Thr	Gly	
	210						215					220					
5	cgc	gga	acc	gtg	gtc	acc	gga	cgt	gtg	gag	cgc	ggc	gtg	atc	aac	gtg	720
	Arg	Gly	Thr	Val	Val	Thr	Gly	Arg	Val	Glu	Arg	Gly	Val	Ile	Asn	Val	
	225					230					235					240	
10	aac	gag	gaa	gtt	gag	atc	gtc	ggc	att	cgc	cca	tcg	acc	acc	aag	acc	768
	Asn	Glu	Glu	Val	Glu	Ile	Val	Gly	Ile	Arg	Pro	Ser	Thr	Thr	Lys	Thr	
					245					250					255		
15	acc	gtc	acc	ggt	gtg	gag	atg	ttc	cgc	aag	ctg	ctc	gac	cag	ggc	cag	816
	Thr	Val	Thr	Gly	Val	Glu	Met	Phe	Arg	Lys	Leu	Leu	Asp	Gln	Gly	Gln	
				260					265					270			
20	gcg	ggc	gac	aac	gtt	ggt	ttg	ctg	ctg	cgg	ggc	gtc	aag	cgc	gag	gac	864
	Ala	Gly	Asp	Asn	Val	Gly	Leu	Leu	Leu	Arg	Gly	Val	Lys	Arg	Glu	Asp	
			275				280						285				
25	gtc	gag	cgt	ggc	cag	gtt	gtc	acc	aag	ccc	ggc	acc	acc	acg	ccg	cac	912
	Val	Glu	Arg	Gly	Gln	Val	Val	Thr	Lys	Pro	Gly	Thr	Thr	Thr	Pro	His	
		290				295					300						
30	acc	gag	ttc	gaa	ggc	cag	gtc	tac	atc	ctg	tcc	aag	gac	gag	ggc	ggc	960
	Thr	Glu	Phe	Glu	Gly	Gln	Val	Tyr	Ile	Leu	Ser	Lys	Asp	Glu	Gly	Gly	
	305				310					315					320		
35	cgg	cac	acg	ccg	ttc	ttc	aac	aac	tac	cgt	ccg	cag	ttc	tac	ttc	cgc	1008
	Arg	His	Thr	Pro	Phe	Phe	Asn	Asn	Tyr	Arg	Pro	Gln	Phe	Tyr	Phe	Arg	
					325					330					335		
40	acc	acc	gac	gtg	acc	ggt	gtg	gtg	aca	ctg	ccg	gag	ggc	acc	gag	atg	1056
	Thr	Thr	Asp	Val	Thr	Gly	Val	Val	Thr	Leu	Pro	Glu	Gly	Thr	Glu	Met	
				340					345					350			
45	gtg	atg	ccc	ggt	gac	aac	acc	aac	atc	tcg	gtg	aag	ttg	atc	cag	ccc	1104
	Val	Met	Pro	Gly	Asp	Asn	Thr	Asn	Ile	Ser	Val	Lys	Leu	Ile	Gln	Pro	
			355				360						365				
50	gtc	gcc	atg	gac	gaa	ggt	ctg	cgt	ttc	gcg	atc	cgc	gag	ggt	ggc	cgc	1152
	Val	Ala	Met	Asp	Glu	Gly	Leu	Arg	Phe	Ala	Ile	Arg	Glu	Gly	Gly	Arg	
		370				375					380						
55	acc	gtg	ggc	gcc	ggc	cgg	gtc	acc	aag	atc	atc	aag	tag				1191
	Thr	Val	Gly	Ala	Gly	Arg	Val	Thr	Lys	Ile	Ile	Lys					
	385				390					395							
60	<210>	14															
	<211>	396															
	<212>	PRT															
	<213>	M. tuberculosis Elongation Factor TU															
	<400>	14															
55	Val	Ala	Lys	Ala	Lys	Phe	Gln	Arg	Thr	Lys	Pro	His	Val	Asn	Ile	Gly	
	1				5					10					15		
60	Thr	Ile	Gly	His	Val	Asp	His	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Ala	Ile	
			20						25					30			
	Thr	Lys	Val	Leu	His	Asp	Lys	Phe	Pro	Asp	Leu	Asn	Glu	Thr	Lys	Ala	

[illegible]

15

	290		295		300
5	Thr Glu Phe Glu Gly Gln Val Tyr Ile Leu Ser Lys Asp Glu Gly Gly				
	305		310		315 320
10	Arg His Thr Pro Phe Phe Asn Asn Tyr Arg Pro Gln Phe Tyr Phe Arg				
		325		330	335
15	Thr Thr Asp Val Thr Gly Val Val Thr Leu Pro Glu Gly Thr Glu Met				
		340		345	350
20	Val Met Pro Gly Asp Asn Thr Asn Ile Ser Val Lys Leu Ile Gln Pro				
		355		360	365
25	Thr Val Gly Ala Gly Arg Val Thr Lys Ile Ile Lys				
	385		390		395
30	<210> 15				
	<211> 17				
	<212> PRT				
	<213> fragment of M. tuberculosis Elongation factor TU				
	<400> 15				
35	Lys Leu Leu Asp Gln Gly Gln Ala Gly Asp Asn Val Gly Leu Leu Leu				
	1	5		10	15
40	Arg				
45	<210> 16				
	<211> 7				
	<212> PRT				
	<213> fragment of P. aeruginosa GroES				
	<400> 16				
50	Leu Arg Pro Leu His Asp Arg				
	1	5			
55	<210> 17				
	<211> 10				
	<212> PRT				
	<213> fragment of P. aeruginosa GroES				
	<400> 17				
60	Gly Glu Val Val Ala Val Gly Thr Gly Arg				
	1	5		10	

16

<210> 18  
 <211> 9  
 <212> PRT  
 5 <213> fragment of P. aeruginosa GroES  
 <400> 18  
 Met Lys Leu Arg Pro Leu His Asp Arg  
 1 5  
 10  
 <210> 19  
 <211> 9  
 <212> PRT  
 15 <213> fragment of P. aeruginosa GroES  
 <400> 19  
 Met Lys Leu Arg Pro Leu His Asp Arg  
 20 1 5  
 <210> 20  
 <211> 13  
 25 <212> PRT  
 <213> fragment of P. aeruginosa GroES  
 <400> 20  
 30 Val Val Phe Gly Pro Tyr Ser Gly Ser Asn Ala Ile Lys  
 1 5 10  
 <210> 21  
 <211> 11  
 35 <212> PRT  
 <213> fragment of P. aeruginosa GroES  
 <400> 21  
 40 Leu Arg Pro Leu His Asp Arg Val Val Ile Arg  
 1 5 10  
 45 <210> 22  
 <211> 13  
 <212> PRT  
 <213> fragment of P. aeruginosa GroES  
 50 <400> 22  
 Val Leu Asp Asn Gly Glu Val Arg Ala Leu Ala Val Lys  
 1 5 10  
 55 <210> 23  
 <211> 17  
 <212> PRT  
 <213> fragment of P. aeruginosa GroES  
 60 <400> 23  
 Thr Ala Gly Gly Ile Val Leu Pro Gly Ser Ala Ala Glu Lys Pro Asn  
 1 5 10 15



17

Arg  
5  
 <210> 24  
 <211> 17  
 <212> PRT  
 10 <213> fragment of P. aeruginosa GroES  
 <400> 24  
 Val Gly Asp Lys Val Val Phe Gly Pro Tyr Ser Gly Ser Asn Ala Ile  
 15 1 5 10 15  
 Lys  
 20  
 <210> 25  
 <211> 97  
 <212> PRT  
 25 <213> P. aeruginosa GroES  
 <400> 25  
 Met Lys Leu Arg Pro Leu His Asp Arg Val Val Ile Arg Arg Ser Glu  
 30 1 5 10 15  
 Glu Glu Thr Lys Thr Ala Gly Gly Ile Val Leu Pro Gly Ser Ala Ala  
 35 20 25 30  
 Glu Lys Pro Asn Arg Gly Glu Val Val Ala Val Gly Thr Gly Arg Val  
 35 40 45  
 40 Leu Asp Asn Gly Glu Val Arg Ala Leu Ala Val Lys Val Gly Asp Lys  
 50 55 60  
 45 Val Val Phe Gly Pro Tyr Ser Gly Ser Asn Ala Ile Lys Val Asp Gly  
 65 70 75 80  
 50 Glu Glu Leu Leu Val Met Gly Glu Ser Glu Ile Leu Ala Val Leu Glu  
 85 90 95  
 Asp  
 55  
 <210> 26  
 <211> 114  
 <212> PRT  
 60 <213> human Calgranulin B  
 <400> 26  
 Met Thr Cys Lys Met Ser Gln Leu Glu Arg Asn Ile Glu Thr Ile Ile

[illegible]